





Taxonomy

Search PubMed ▼ for

Protein

PopSet Go Clear OMIN

Limits

Preview/Index

☐ 1: Biochim Biophys Acta 1993 May 13:1163

History

Clipboard

Deta

LinkOut

About Entrez

Display **Abstract**

(2):113-23

Sort

Cip Add

Related Articles, Books,

Text Version

Entrez PubMed Overview Help | FAQ Tutorial New/Noteworthy

PubMed Services Journal Browser MeSH Browser Single Citation Matcher **Batch Citation Matcher** Clinical Queries LinkOut Cubby

Related Resources Order Documents **NLM Gateway** TOXNET Consumer Health Clinical Alerts ClinicalTrials.gov PubMed Central

Privacy Policy

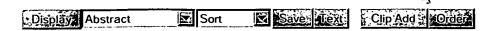
Estimation of the secondary structure and conformation of bovine lens crystallins by infrared spectroscopy: quantitative analysis and resolution by Fourier self-deconvolution and curve fit.

Lamba OP, Borchman D, Sinha SK, Shah J, Renugopalakrishnan V, Yappert MC.

Department of Ophthalmology and Visual Sciences, University of Louisville School of Medicine, Kentucky Lions Eye Research Institute 40292.

The secondary structure of six bovine lens protein fractions (two alpha, three beta and one gamma-crystallin) are examined in solution and in solid forms for the first time using FTIR spectroscopy. Films of the nuclear and cortical regions of the bovine lens are also examined. The structure is quantitatively estimated from the vibrational analysis of the resolution-enhanced amide-I profile achieved by Fourier selfdeconvolution and linear least-squares curve-fit algorithm. All the protein fractions fold predominantly in a beta-pleated sheet structure with little or no alpha-helical domains in solution or in lyophilized solid form. These proteins also retain their predominant beta-sheet conformation in the cellular phospholipid environment of the lens, in conformity with the structure obtained for all the mammalian species examined to date. Despite structural homology, vibrational data indicate subtle structural differences within each class of the crystallins probably due to presence of several minor substructures/subconformations. Substantial high amounts of turns (approx. 40%) observed in the betafractions may have a fundamental implication in stabilizing the tertiary structure of the uniquely folded-proteins vital for the transparency of the lens. These proteins in solid KBr-matrix undergo a major structural change, induced primarily by ionic interactions which refold them in a helical conformation. IR spectroscopy together with band-narrowing procedures has proven to be an effective tool to obtain structural information of proteins in solution, as solid substrates or in a complex biological tissue, such as ocular lens.

PMID: 8490044 [PubMed - indexed for MEDLINE]



Write to the Help Desk
NCBI | NLM | NIH
Department of Health & Human Services
Freedom of Information Act | Disclaimer

spare-sun-solaris2.8 May 10 2002 11:21:51